



Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

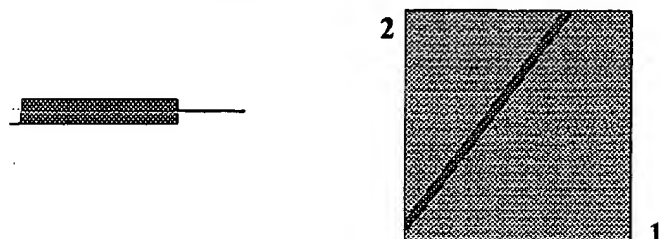
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.6 [Apr-09-2003]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: ☐ Filter ☐ Align

Sequence 1 lcl|seq_1

Length 1910 (1 .. 1910)

Sequence 2 gi 3360444 Homo sapiens clone 23625 mRNA sequence Length 1462 (1 .. 1462)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 2607 bits (1356), Expect = 0.0
 Identities = 1356/1356 (100%)
 Strand = Plus / Plus



```

Query: 1      cttggtcctgatgtctgaccatggagatgtgagcctcccgcccgaagaccgggtgagggc 60
              |||
Sbjct: 107    cttggtcctgatgtctgaccatggagatgtgagcctcccgcccgaagaccgggtgagggc 166

Query: 61      tctctcccagctgggtagtgcggtagaggtgaatgaagacattccaccccgtcggtactt 120
              |||
Sbjct: 167    tctctcccagctgggtagtgcggtagaggtgaatgaagacattccaccccgtcggtactt 226

Query: 121     ccgctctggagttgagattatccgaatggcatccatttactctgaggaaggcaacattga 180
              |||
Sbjct: 227     ccgctctggagttgagattatccgaatggcatccatttactctgaggaaggcaacattga 286

Query: 181     acatgccttcacctctataacaagtatatcacgctctttattgagaaactacaaaaca 240
              |||
Sbjct: 287     acatgccttcacctctataacaagtatatcacgctctttattgagaaactacaaaaca 346

Query: 241     tcgagattacaaatctgctgtcattcctgaaaagaaagacacagtaagaaattaaagga 300
              |||
Sbjct: 347     tcgagattacaaatctgctgtcattcctgaaaagaaagacacagtaagaaattaaagga 406
    
```

Query: 301 gattgcatttcccaaagcagaagagctgaaggcagagctgtttaaaccgatataccaaaga 360
|||||
Sbjct: 407 gattgcatttcccaaagcagaagagctgaaggcagagctgtttaaaccgatataccaaaga 466

Query: 361 atatacagaatataatgaagaaaagaagaaggaagcagaggaattggcccgaacatggc 420
|||||
Sbjct: 467 atatacagaatataatgaagaaaagaagaaggaagcagaggaattggcccgaacatggc 526

Query: 421 catccagcaagagctggaaaaggaaaaacagagggtagcacaacagaagcagcagcaatt 480
|||||
Sbjct: 527 catccagcaagagctggaaaaggaaaaacagagggtagcacaacagaagcagcagcaatt 586

Query: 481 ggaacaggaacagttccatgccttcgaggagatgatccggaaccaggagctagaaaaaga 540
|||||
Sbjct: 587 ggaacaggaacagttccatgccttcgaggagatgatccggaaccaggagctagaaaaaga 646

Query: 541 gcgactgaaaattgtacaggagtttgggaaggtagaccctggcctaggtggcccgtagt 600
|||||
Sbjct: 647 gcgactgaaaattgtacaggagtttgggaaggtagaccctggcctaggtggcccgtagt 706

Query: 601 gcctgacttgagaagccctccttagatgtgttccccaccttaacagtctcatccataca 660
|||||
Sbjct: 707 gcctgacttgagaagccctccttagatgtgttccccaccttaacagtctcatccataca 766

Query: 661 gccttcagactgtcacacaactgtaaggccagctaagccacctgtggtggacaggtcctt 720
|||||
Sbjct: 767 gccttcagactgtcacacaactgtaaggccagctaagccacctgtggtggacaggtcctt 826

Query: 721 gaaacctggagcactgagcaactcagaaagtattcccacaatcgatggattgcgccatgt 780
|||||
Sbjct: 827 gaaacctggagcactgagcaactcagaaagtattcccacaatcgatggattgcgccatgt 886

Query: 781 ggtggtgcctgggcggtgtgtgccacagtttctccagttagccagtgccaaactgcccg 840
|||||
Sbjct: 887 ggtggtgcctgggcggtgtgtgccacagtttctccagttagccagtgccaaactgcccg 946

Query: 841 gggagtggagacatgtggaattctctgtggaaaactgatgaggaatgaatttaccattac 900
|||||
Sbjct: 947 gggagtggagacatgtggaattctctgtggaaaactgatgaggaatgaatttaccattac 1006

Query: 901 ccatgttctcatccccaagcaaagtgtggtctgattactgcaacacagagaacgaaga 960
|||||
Sbjct: 1007 ccatgttctcatccccaagcaaagtgtggtctgattactgcaacacagagaacgaaga 1066

Query: 961 agaacttttctcatcacaggatcagcagggcctcatcacactgggctggattcatactca 1020
|||||
Sbjct: 1067 agaacttttctcatcacaggatcagcagggcctcatcacactgggctggattcatactca 1126

Query: 1021 cccacacagaccggtttctctccagtgtcgacctacacactcactgctcttaccagat 1080
|||||
Sbjct: 1127 cccacacagaccggtttctctccagtgtcgacctacacactcactgctcttaccagat 1186

Query: 1081 gatgttgccagagtcagtagccattgtttgctcccccaggtccaggaaactggattctt 1140
|||||
Sbjct: 1187 gatgttgccagagtcagtagccattgtttgctcccccaggtccaggaaactggattctt 1246

Query: 1141 taaactaactgaccatggactagaggagatttcttcctgtcgccagaaaggatttcatcc 1200
|||||
Sbjct: 1247 taaactaactgaccatggactagaggagatttcttcctgtcgccagaaaggatttcatcc 1306

Query: 1201 acacagcaaggatccacctctgttctgtagctgcagccacgtgactggttggtggacagagc 1260
|||||
Sbjct: 1307 acacagcaaggatccacctctgttctgtagctgcagccacgtgactggttggtggacagagc 1366

Query: 1261 agtgaccatcacagaccttcgatgagcgtttgagtccaacaccttccaagaacaacaaaa 1320
|||||
Sbjct: 1367 agtgaccatcacagaccttcgatgagcgtttgagtccaacaccttccaagaacaacaaaa 1426

Query: 1321 ccatatcagtgtactgttagcccccttaatttaagctt 1356
|||||
Sbjct: 1427 ccatatcagtgtactgttagcccccttaatttaagctt 1462

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

| Lambda | K | H |
|--------|-------|------|
| 1.33 | 0.621 | 1.12 |

| Gapped Lambda | K | H |
|------------------|-------|------|
| 1.33 | 0.621 | 1.12 |

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 3
Number of Sequences: 0
Number of extensions: 3
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 1462
length of database: 9,515,983,914
effective HSP length: 25
effective length of query: 1437
effective length of database: 9,515,983,889
effective search space: 13674468848493
effective search space used: 13674468848493
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)